Figure 1

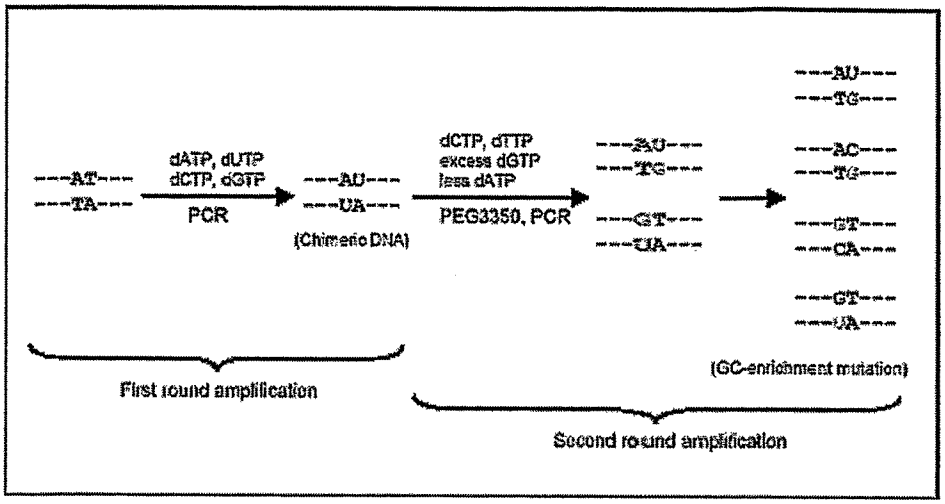

Figure 2

	34						38			41					103		105		107		
AlbD	-R	C	I	L	F	A	A	G	L	S	G	-	-	-	G	V	G	H	S	L	G	S	V-
Bhc	-R	A	V	L	L	L	H	G	F	T	G	-	-	-	V	G	G	L	S	L	G	G	V-
Sac	-R	A	V	L	L	L	H	G	F	T	G	-	-	-	V	A	G	L	S	L	G	G	D-
Lic	-R	A	V	L	L	L	H	G	F	T	G	-	-	-	I	I	G	F	S	M	G	G	V-
Bsc	-K	A	V	L	L	L	H	G	F	T	G	-	-	-	A	C	G	L	S	L	G	G	V-
Tme	-K	G	V	L	F	I	H	G	Y	T	G	-	-	-	I	I	G	F	S	M	G	G	V-
Tpc	-H	A	V	L	L	I	H	G	Y	M	G	-	-	-	V	G	G	L	S	M	G	G	V-
Pcl	-Y	P	I	I	L	Y	H	G	L	T	G	-	-	-	L	V	G	H	S	Q	G	G	Q-
Bsc	-A	P	L	V	L	L	H	G	F	T	G	-	-	-	I	I	A	H	S	Q	G	G	Q-
Consensus				L	x	x	x	G	x	x	G						G	x	S	x	G		
				(I)													(A)						
				(V)																			

Figure 3

MDKSDLTETSRIKHGEEAFDVTLLQVKGATRCILFAAGLGGSPLRHLELLQ
TFARHGVSVVAPHFERLTSPVPTRAELLERCQRLARAQNEFCSGYASVTGV
GHSLGSVILLLNAGAIAMTSAGESVVFAGDRMLHRLILLAPPADFFQAPSA
LAAVNVPVHIWAGEKDSLTPPSQACFLKQALEGYTQTYLCVMEEAGHFTFM
NTLPPQVTDSHPSREAFLLDLGENIARLVTD

Figure 4

ATGGACAAAAGTGATCTCACGGAAACGTCTCGGATCAAACATGGGGAAGAG
GCGTTTGACGTCACCTTATTGCAGGTTAAGGGGGCGACGCGCTGTATCCTT
TTTGCTGCGGGGCTGGGCGGCAGTCCGCTGCGCCATCTTGAACTTCTCCAG
ACCTTTGCCCGCCATGGCGTTTCCGTTGTCGCGCCACACTTTGAACGGTTG
ACCTCACCCGTGCCCACCAGAGCTGAATTACTGGAACGCTGCCAGCGGCTT
GCGCGGGCTCAGAATGAATTTTGTAGCGGTTATGCGTCGGTTACCGGTGTT
GGCCACTCCCTGGGTAGCGTGATTTTATTGCTGAATGCCGGGGCTATAGCG
ATGACAAGCGCAGGGGAATCGGTTGTTTTCGCCGGCGACCGGATGTTGCAT
CGACTTATTTTACTGGCACCGCCCGCCGATTTTTTCCAGGCTCCGTCTGCG
CTGGCAGCGGTGAACGTACCTGTTCACATCTGGGCAGGTGAAAAGGACAGC
CTGACGCCCCCGTCCCAGGCCTGCTTTCTTAAACAGGCACTGGAGGGTTAC
ACGCAGACTTATCTCTGTGTGATGGAAGAGGCCGGGCATTTTACCTTCATG
AATACCTTGCCTCCGCAGGTAACCGATTCACATCCGTCGCGGGAGGCCTTT
CTTTTAGATTTGGGCGAAAACATAGCCCGGCTGGTGACTGAT